version -

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Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds.
U49250 S78865
U49250.1 GI:1222542
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Bulfone,A., Smiga,S.M., Shimamura,K., Peterson,A., Puelles,L. and Rubenstein,J.L.
T-brain-1: a homolog of Brachyury whose expression defines molecularly distinct domains within the cerebral cortex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION: U49250
ACCESSION: U49251
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                                                                                               March 2, 2006, 15:19:36 7, Search time 6 Seconds (without alignments) 3.595 Million cell updates/sec
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Direct Submission
Submitted (15-FEB-1996) Susan M. Smiga, Psychiatry, UCSF, 401
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 5.1.7
Biocceleration Ltd
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2: /home/njarrell/juedes264/mmu49251.gb_ro:*
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                                                                  OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 2 summaries
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MMU49251
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GenCore
Copyright (c) 1993
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Maximum DB seq length: 2000000000
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/fbsue type="brain"
/clone_lib="17 week fetal brain cDNA library (Stratagene)"
/dev stage="17 week fetus"
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RHQTEMI ITKQGRRMFPFLSFNI SGLDPTAHYNI FVDVILADPNHWRPQGGKWVPCGK
ADTNVQGNRVYMHPDSPNTGAHWMRQEI SFGKLKLTINNKGASNNNGQMVVLQSLHKYQ
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NDTD1YTGCOMBLLIPSPNDSPRSQ1VGARYAMAGSFLQDQPSVRYAKARPHEGAG
AGPGPGTDRSVPHTRGLLSPQAGDPGAPSQRWFVTPANNRLDFAASAYDTATDFAG
NAATLLSYAAAGVKALPLQAAGCTGRPLGYYDDSGWARSPPQYCGTKGGSYLLEVW
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NLERSSPLKKITRGMTNQSDTDNFPDSKDSPGDVQRSKLSPVLDGVSELRHSFDGSAA
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DSSDSGIYEQAKRRRISPADTPVSESSSPLKSEVLAQRDCEKNCAKDISGYYGFYSHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="putative transcriptional regulator; T-box brain gene; Tes-56"
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                                    , 1996 this sequence version replaced gi:1042025.
Location/Qualifiers
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Pred. No. 0;
0; Mismatches 367;
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Parnassus Avenue, SF, CA 94143,
On Mar 12, 1996 this sequence ve
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3814)
Bulfone, A., Smiga, S.M., Shimamura, K., Peterson, A., Puelles, L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="putative transcriptional regulator; T-box brain
gene; Tes-56"
                                                                                                                                                                                                                 863 ATGTGCAAGGAAATCGGGTCTATATGCATCCGGATTCCCCCAACACTGGGGCTCACTGGA
                                                                       923 TGCGCCAAGAAATCTCTTTTGGAAAATTAAAACTTACGAACAACAAAAAAGGAGCTTCAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                      cortex transcriptional regulator
                                                /note="First 8 base pair were sequenced from genomic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (15-FEB-1996) Susan M. Smiga, Psychiatry, UCSF, 401
Parnassus Avenue, SF, CA 94143, USA
On Mar 12, 1996 this sequence version replaced gi:1042023.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rubenstein, J.L.
T-brain-1: a homolog of Brachyury whose expression defines
molecularly distinct domains within the cerebral cortex
Neuron 15 (1), 63-78 (1995)
                                                                                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus putative cerebral cortex T-Brain-1 (Tbr-1) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                    CATCTGTTGACACCAGCATCCCCTCCCC 1025
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chromosome="2"
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/product="T-Brain-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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AGGPGFTDRSVPHTWGLLSPQQAEDPGAPSPQWWFVTPANNRLDFAAAYDTATDFAG
NAATLLSYAAGVKALPLQAGCTGRPLGYYADPSGWGARSPPQYCGAKSGSVLPCWP
NSAAAARWAGANPTJGERAGGLAARSPLARABDAKFKDLSDSSWIETPSSIKSID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 GGCTTCCCCGGCGCGGCGAGTCCTTCCCGCCGCGGGCGACGCCGAGGGCTACCAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGAGGGCTACGCCGCCCGGACCCGGCGCCCGGGCTCTACCCGGGCCCGCGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       decidentacectracidades de la contración d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccacttricecteaaatittcatceecatcaaaceeagateatcatcactaaacaeeaaee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cecaretraccertrareagritraacatraciesteseareceareceareagrand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTCCTTGTGGCAAAGCGGACACCAATGTGCAAGGAAACCGGGTCTATATGCATCCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                489 ccesicionarica contrator de contrator de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        549 ATTACCAACGGAGCTTACAACAGCCTGCTCTCCAACTCTTCGCCGCAGGGCTACCCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 TACGCGCTACCCGCGGGACTGGAGGTGTCGGGGAAACTGAGGGTCGCGCTCAACAACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGCCCCCCCCCCCTCCCTTGGAGCCTACGCCTACCCGCCGCGAACCCCAGGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 313.999; DB 2
Pred. No. 0;
0; Mismatches 335;
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Best Local Similarity 60.6
Matches 515; Conservative
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1269 CGAGATAACTATGACACGATCTACACGGGCTGCGACATGGACCGCTTGACCCCGTCGCCC 1328 g

1033 CCCAACTGTC 1042 | | | | | | | 1329 AACGACTCTC 1338 g

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Search completed: March 2, 2006, 15:19:43 Job time: 7 secs